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RAW SEQUENCE LISTING

DATE: 06/28/2002

PATENT APPLICATION: US/10/007,527A

TIME: 11:20:06

Input Set : A:\CL1709 US NA SEQ.txt

Output Set: N:\CRF3\06282002\J007527A.raw

5 <110> APPLICANT: Tomb, Jean-Francois
6 Bramucci, Michael G.
7 Cheng, Qiong
8 Kostichka, Kristy N.
11 <120> TITLE OF INVENTION: Rhodococcus Cloning and Expression Vectors
14 <130> FILE REFERENCE: CL1709 US NA
C--> 17 <140> CURRENT APPLICATION NUMBER: US/10/007,527A
C--> 17 <141> CURRENT FILING DATE: 2001-12-05
17 <150> PRIOR APPLICATION NUMBER: 60/254,868
18 <151> PRIOR FILING DATE: 2000-12-12
21 <160> NUMBER OF SEQ ID NOS: 30
24 <170> SOFTWARE: Microsoft Office 97
27 <210> SEQ ID NO: 1
29 <211> LENGTH: 1140
31 <212> TYPE: DNA
33 <213> ORGANISM: Rhodococcus AN12
37 <400> SEQUENCE: 1

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42	gaaacattta	acgctgttgg	ccggccgatt	tctggcgtga	acggtgtgac	cattgtcaac	180
44	ggtccgaaa	ggtctggatt	cggaggcctt	cgttcctgcg	gaaagggctg	gatctgcccc	240
46	tgctgtgcgg	gaaaagtgcg	tgcacatcgt	gcagacgaaa	tttctcaagt	tgttgctcat	300
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50	cggctccacg	acctatggac	tggactttcg	gcagcctgga	aagctgcgac	caacggtcgt	420
52	cgttggcgta	cggaaacgtga	aatgtacggc	tgcgacggat	acgtgcgcgc	tgttgaaatc	480
54	actcacggaa	aaaacggctg	gcacgtccac	gttcacgcgc	tactcatgtt	cagtgggtgac	540
56	gtgagtgaga	acatcctcga	atccttctcg	gatgcgatgt	tcgatcgggtg	gacttccaaa	600
58	ctcgtatctc	tgggatttgc	tgcgccacta	cgtaattcgg	gtggtctcga	tgtacgaaag	660
60	atcggcgggtg	aagctgatca	agttctcgtc	gcgtatctga	cgaaaattgc	atctggcggt	720
62	ggtatggagg	ttggtagtgg	cgacggaaaa	agtggtcgac	atggcaaccg	tgcaccctgg	780
64	gaaatcgctg	ttgatgcagt	gggcggggat	ccacaagcgt	tggaactgtg	gcgagaattt	840
66	gagtttggtt	cgatgggacg	tcgggcaatc	gcgtggtccc	gtggattgcg	tgcccagagct	900
68	ggtcttgggg	cagaactaac	agatgctcag	atcgttgagc	aggaagaatc	tgccccggtc	960
70	atggttgcca	tcattccggc	gcgatcgtgg	atgatgattc	ggacttgtgc	gccttacgtc	1020
72	ttcggcgaga	tcctcggact	cgtcgaagct	ggcgcgactt	gggaaaatct	tcgtgatcac	1080
74	ttgcattatc	gattgcocgc	agcggatgtg	cggcccccca	taatatcggt	tcgcaagtga	1140

77 <210> SEQ ID NO: 2
79 <211> LENGTH: 379
81 <212> TYPE: PRT
83 <213> ORGANISM: Rhodococcus AN12
87 <400> SEQUENCE: 2

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97 Lys Leu Gln Gln Ile Thr Thr Ser Glu Thr Phe Asn Ala Cys Gly Arg
98          35          40          45
101 Pro Ile Ser Gly Val Asn Gly Val Thr Ile Val Asn Gly Pro Lys Gly
102          50          55          60
105 Ser Gly Phe Gly Gly Leu Arg Ser Cys Gly Lys Gly Trp Ile Cys Pro
106 65          70          75          80
109 Cys Cys Ala Gly Lys Val Gly Ala His Arg Ala Asp Glu Ile Ser Gln
110          85          90          95
113 Val Val Ala His Gln Leu Gly Thr Gly Ser Val Ala Met Val Thr Met
114          100          105          110
117 Thr Met Arg His Thr Ala Gly Gln Arg Leu His Asp Leu Trp Thr Gly
118          115          120          125
121 Leu Ser Ala Ala Trp Lys Ala Ala Thr Asn Gly Arg Arg Trp Arg Thr
122          130          135          140
125 Glu Arg Glu Met Tyr Gly Cys Asp Gly Tyr Val Arg Ala Val Glu Ile
126 145          150          155          160
129 Thr His Gly Lys Asn Gly Trp His Val His Val His Ala Leu Leu Met
130          165          170          175
133 Phe Ser Gly Asp Val Ser Glu Asn Ile Leu Glu Ser Phe Ser Asp Ala
134          180          185          190
137 Met Phe Asp Arg Trp Thr Ser Lys Leu Val Ser Leu Gly Phe Ala Ala
138          195          200          205
141 Pro Leu Arg Asn Ser Gly Gly Leu Asp Val Arg Lys Ile Gly Gly Glu
142          210          215          220
145 Ala Asp Gln Val Leu Ala Ala Tyr Leu Thr Lys Ile Ala Ser Gly Val
146 225          230          235          240
149 Gly Met Glu Val Gly Ser Gly Asp Gly Lys Ser Gly Arg His Gly Asn
150          245          250          255
153 Arg Ala Pro Trp Glu Ile Ala Val Asp Ala Val Gly Gly Asp Pro Gln
154          260          265          270
157 Ala Leu Glu Leu Trp Arg Glu Phe Glu Phe Gly Ser Met Gly Arg Arg
158          275          280          285
161 Ala Ile Ala Trp Ser Arg Gly Leu Arg Ala Arg Ala Gly Leu Gly Ala
162          290          295          300
165 Glu Leu Thr Asp Ala Gln Ile Val Glu Gln Glu Glu Ser Ala Pro Val
166 305          310          315          320
169 Met Val Ala Ile Ile Pro Ala Arg Ser Trp Met Met Ile Arg Thr Cys
170          325          330          335
173 Ala Pro Tyr Val Phe Gly Glu Ile Leu Gly Leu Val Glu Ala Gly Ala
174          340          345          350
177 Thr Trp Glu Asn Leu Arg Asp His Leu His Tyr Arg Leu Pro Ala Ala
178          355          360          365
181 Asp Val Arg Pro Pro Ile Ile Ser Val Arg Lys
182          370          375
185 <210> SEQ ID NO: 3
187 <211> LENGTH: 891
189 <212> TYPE: DNA

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200 aaatctcaat gcacctacaa cctgtctgca caggctggat cgaatcccgc tgtgctgtc      180
202 gtcggagtcg atcccacttc cgtcttacta gccccattcg tccaccgacg accggctgaa      240
204 ccgaacatcg agctcgggct gaacgatttt gacaaagtcc tccgagtgtc ccagttcgtc      300
206 aaagcagaat ctgaccgacg aatcgagtgt ttctgggata gacgcataga caaaatttcg      360
208 ttgttctcgc cagcactacc tctcatcctg ctctgtactg aagaatttcc cggaatcatc      420
210 gagggcgcac aggatttcga tgcaaccaac ggtctgaaac cagcagacag atacgcaccc      480
212 cgcatacatc cgcttggttc acagatcgct gctcagtcgt ccaaagcagg catcagaatg      540
214 ttgctcttgg ctcaacgtgc ggaagcttcc atcgtgggtg gaaacgcccg ctggaacttc      600
216 gcggtgaaaa tgactctccg cgtagacgaa cctgaatctg tcaaaatgct gcaccccaac      660
218 gcaacacctg aagagtgcgc actggctgaa ggattcgtcc ctggtcaagg cttcttcgac      720
220 caacccggac tacggcgcca aatgatccga acggttcgcg taggtgagta ctcgacctac      780
222 gcgagttacg tcgaaaacgc agacctcgcg tacgaagccg cactgaacat cgaccgagca      840
224 caacgaatga caatgcctc  ggaataccca catctcggcg acataggctg a      891
227 <210> SEQ ID NO: 4
229 <211> LENGTH: 296
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237 <400> SEQUENCE: 4
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243 Ala Gln Pro Val Met Val Asp Ile Ala Lys Asp Ala Ala His Trp Leu
244 20 25 30
247 Ile Gln Gly Lys Thr Arg Ser Gly Lys Ser Gln Cys Thr Tyr Asn Leu
248 35 40 45
251 Leu Ala Gln Ala Gly Ser Asn Pro Ala Val Arg Val Val Gly Val Asp
252 50 55 60
255 Pro Thr Ser Val Leu Leu Ala Pro Phe Val His Arg Arg Pro Ala Glu
256 65 70 75 80
259 Pro Asn Ile Glu Leu Gly Leu Asn Asp Phe Asp Lys Val Leu Arg Val
260 85 90 95
263 Leu Gln Phe Val Lys Ala Glu Ser Asp Arg Arg Ile Glu Cys Phe Trp
264 100 105 110
267 Asp Arg Arg Ile Asp Lys Ile Ser Leu Phe Ser Pro Ala Leu Pro Leu
268 115 120 125
271 Ile Leu Leu Val Leu Glu Glu Phe Pro Gly Ile Ile Glu Gly Ala Gln
272 130 135 140
275 Asp Phe Asp Ala Thr Asn Gly Leu Lys Pro Ala Asp Arg Tyr Ala Pro
276 145 150 155 160
279 Arg Ile Thr Ser Leu Val Arg Gln Ile Ala Ala Gln Ser Ala Lys Ala
280 165 170 175
283 Gly Ile Arg Met Leu Leu Leu Ala Gln Arg Ala Glu Ala Ser Ile Val
284 180 185 190
287 Gly Gly Asn Ala Arg Ser Asn Phe Ala Val Lys Met Thr Leu Arg Val
288 195 200 205
291 Asp Glu Pro Glu Ser Val Lys Met Leu His Pro Asn Ala Thr Pro Glu

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292      210      215      220
295 Glu Cys Ala Leu Val Glu Gly Phe Val Pro Gly Gln Gly Phe Phe Asp
296 225      230      235      240
299 Gln Pro Gly Leu Arg Arg Gln Met Ile Arg Thr Val Arg Val Gly Glu
300      245      250      255
303 Tyr Ser Thr Tyr Ala Ser Tyr Val Glu Asn Ala Asp Leu Ala Tyr Glu
304      260      265      270
307 Ala Ala Leu Asn Ile Asp Arg Ala Gln Arg Met Thr Ile Ala Ser Glu
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330 ggaaccaaat tctccactgt gatggatagt gcgagacgat ccatgccagt catgtagggc      180
332 tgcaccacaga caaggccttc tgctcggtag atcgtgccga agctgaacgg ctcggttcggc      240
334 gggttgatga cgtgcacgga tgctgtcttg tcagtcgcaa cagttccgtc cttgcttgca      300
336 actcgagaca atgcgccagt cgaatacttc acacggccgt cgggagttag cttgtcctga      360
338 accggcttga tggggtcgtc cataccggct acgaacaccg ggaactgata agcggtagtt      420
340 gcgacgggga gggacgttcc gagctgaaca ttcatgcgag ttcccttgat cgaggctggt      480
342 acagcttatg tctccggtgt ccatattcag cgacacgcgt tcattctacac tcaaaaccgt      540
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354 aactgcctct gagctgcgca aatctatttc ccgttttctc gttgacgagc ttgacgtcag      900
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366 gaacgcatca tctcgatcca gcgtggtttc ttgaccataa atcgagaggt acacgcccatt      1260
368 gacaacgcca tcgacgtcta ccgaagctgg attcgtctcg atgccaagag gacgttcggt      1320
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384 cagccccccg agaccaacca tgaaacaggc cgtctctctg tcaaggccaa gccgctacgc      1800
386 ggtgctatcg cagccctgac agagagacac ccagcttcag agcggcaagt atcgggggga      1860
388 tgccctcaag tgtggttcat gggggtgaaa gttgttgctc agcaacgctt ttcacttgcg      1920
390 aaccgatatt atcgggggcc gcacatccgc tgcgggcaat cgataatgca agtgatcacg      1980

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VERIFICATION SUMMARY

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L:17 M:271 C: Current Filing Date differs, Replaced Current Filing Date